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5' Tyr Leu Tyr Gln Trp Leu Gly Ala Pro Val Pro
 TAC CTG TAT CAA TGG CTG GGA GCC CCA GTC CCC
 Tyr Pro Asp Pro Leu Glu Pro Arg Arg Glu Val
 TAC CCG GAT CCC CTG GAG CCC AGG AGG GAG GTG
 Cys Glu Leu Asn Pro Asp Cys Asp Glu Leu Ala
 TGT GAG CTC AAT CCG GAC TGT GAC GAG TTG GCT
 Asp His Ile Gly Phe Gln Glu Ala Tyr Arg Arg
 GAC CAC ATC GGC TTT CAG GAG GCC TAT CGG CGC
 Phe Tyr Gly Pro Val stop PstI
 TTC TAC GGC CCG GTC TAA CTG CAG ATGC 3'

FIG. 1A

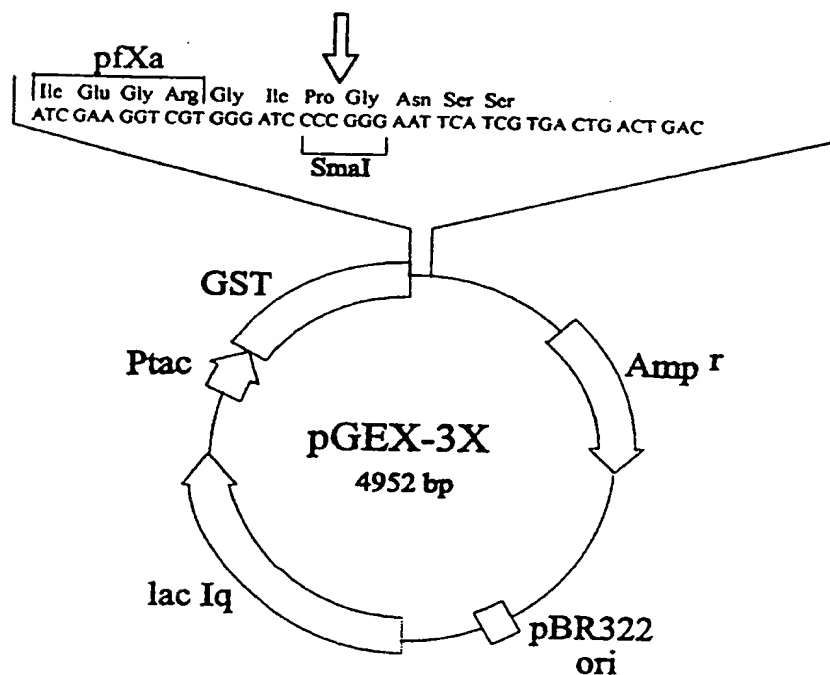


FIG. 1B

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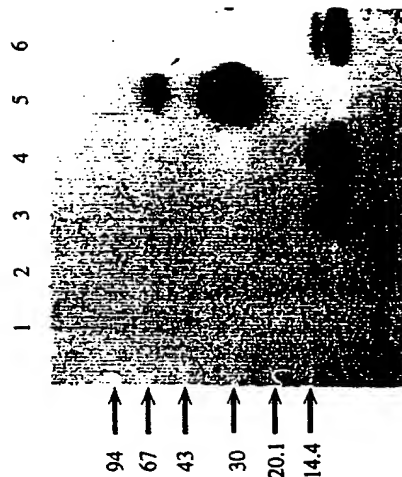


FIG. 2B

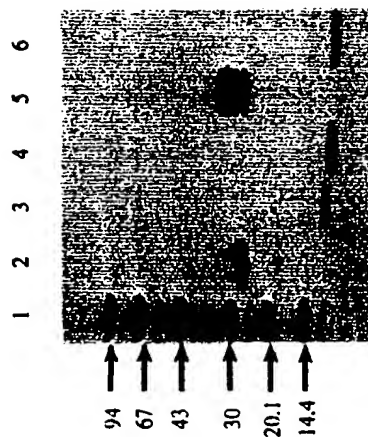


FIG. 2A

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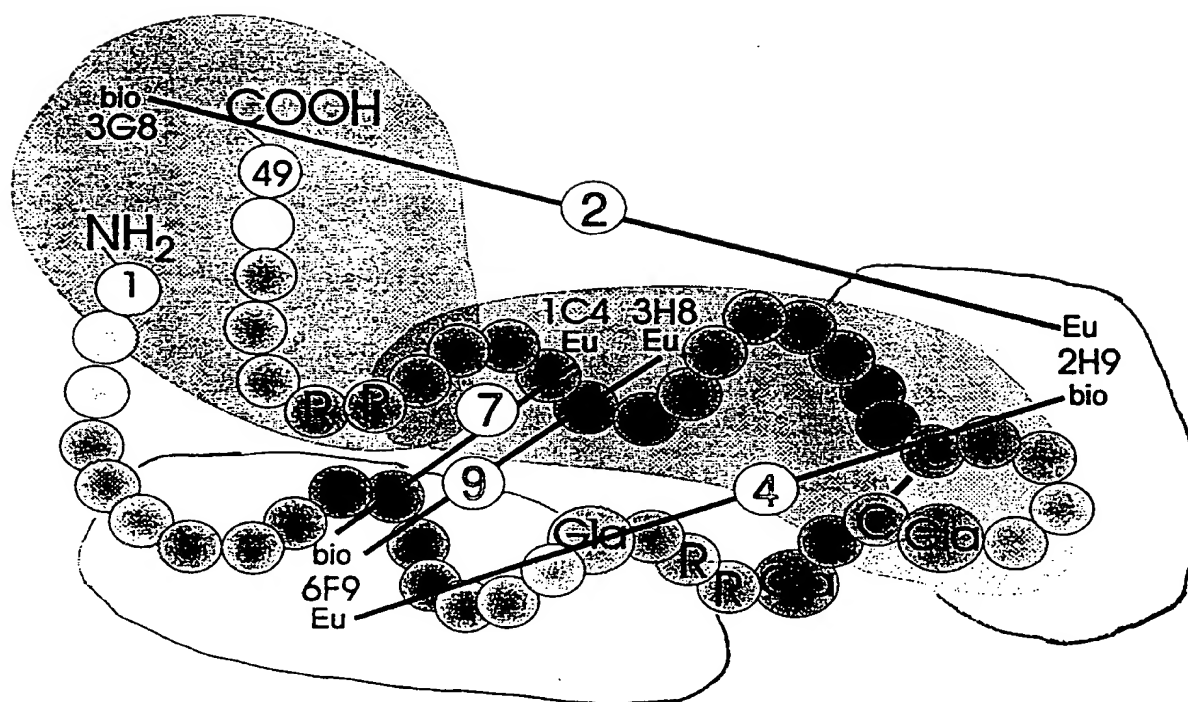


FIG.3

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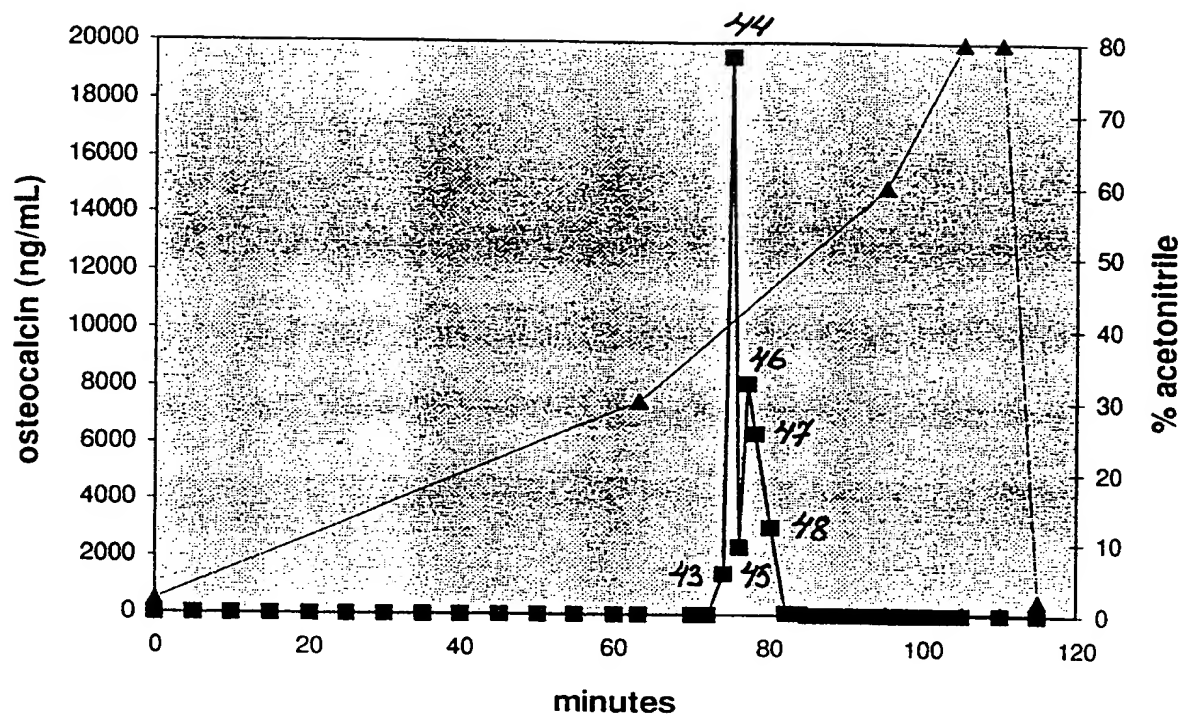
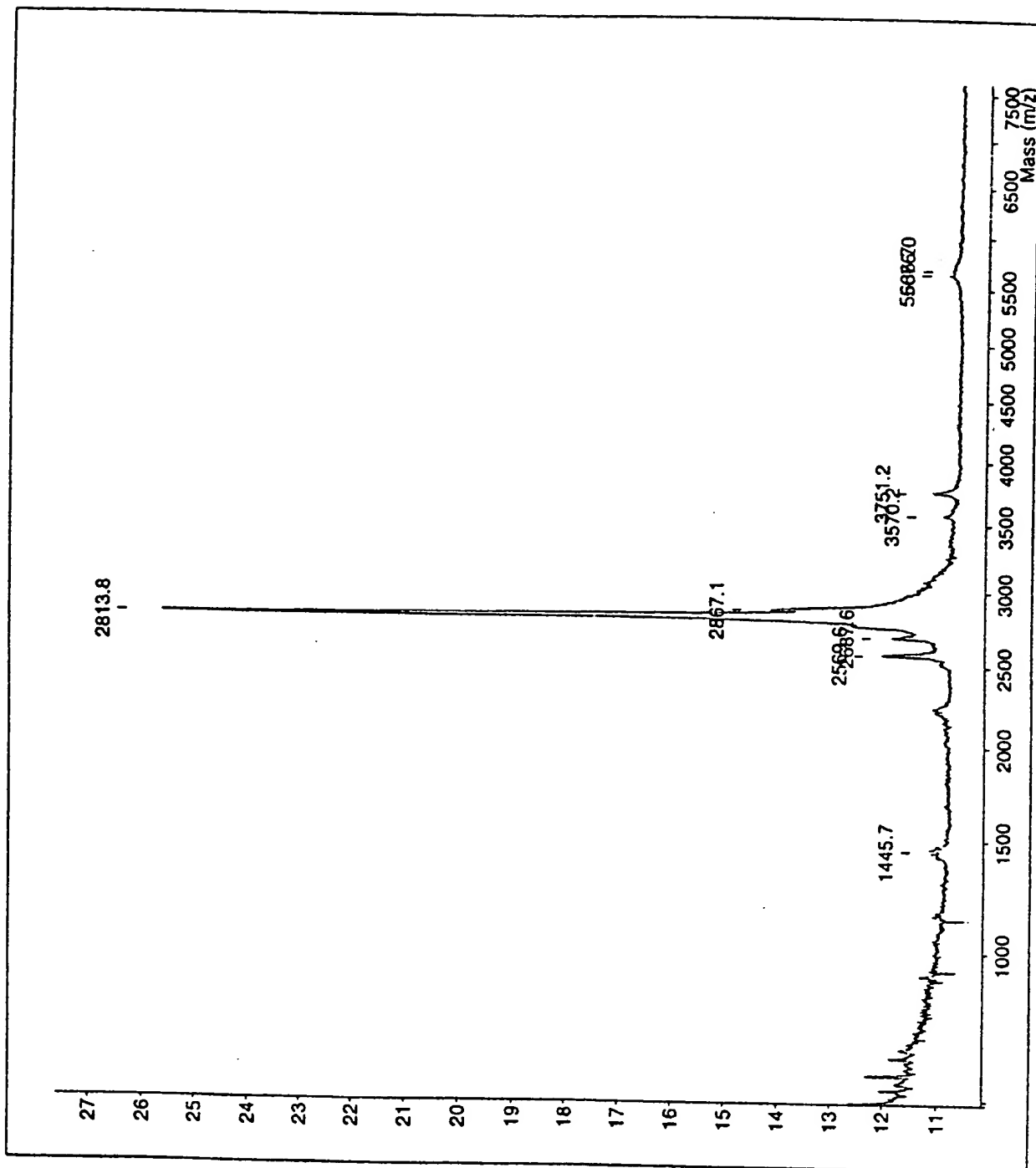


FIG. 4

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FIG. 5A



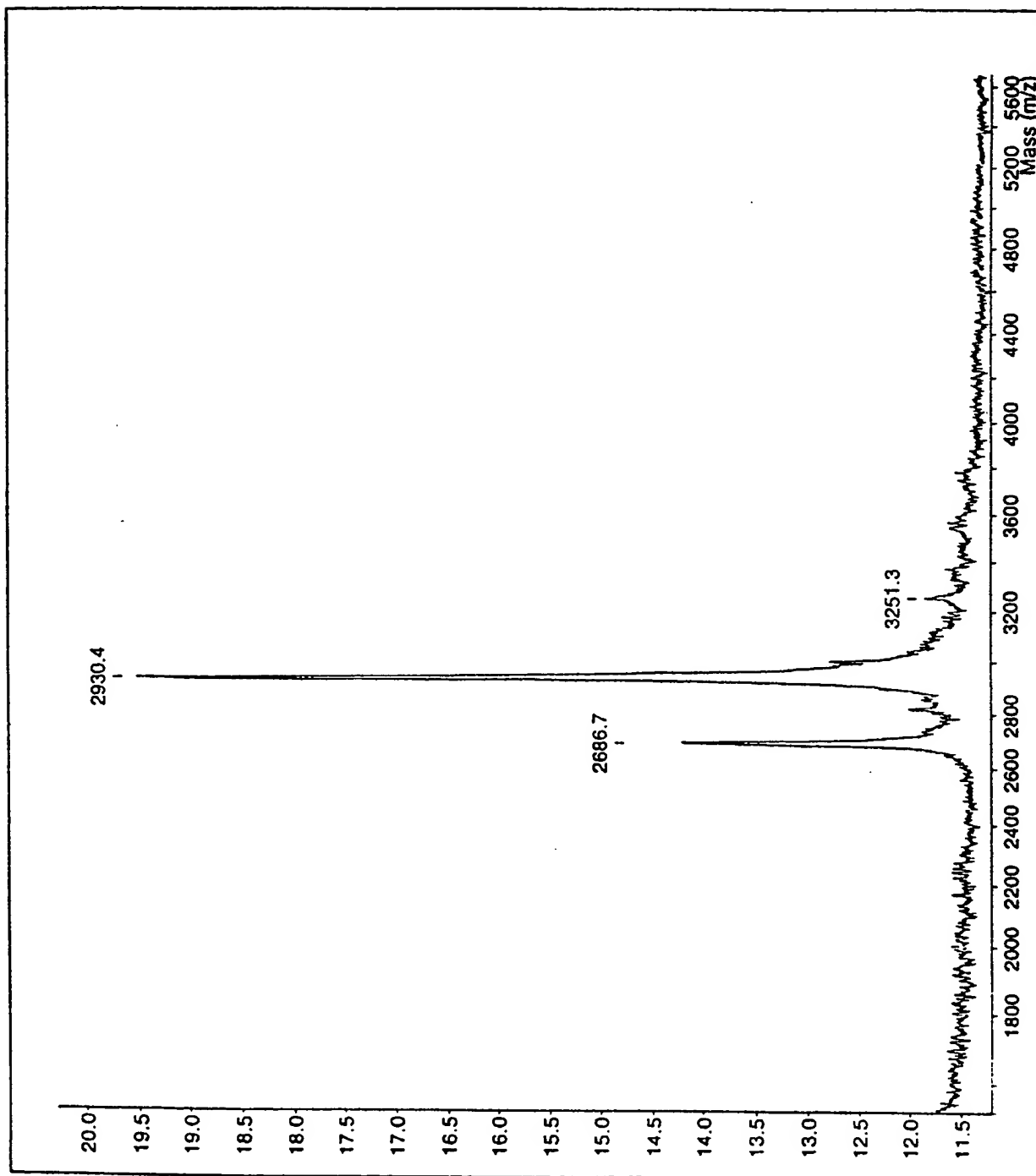


FIG. 5B

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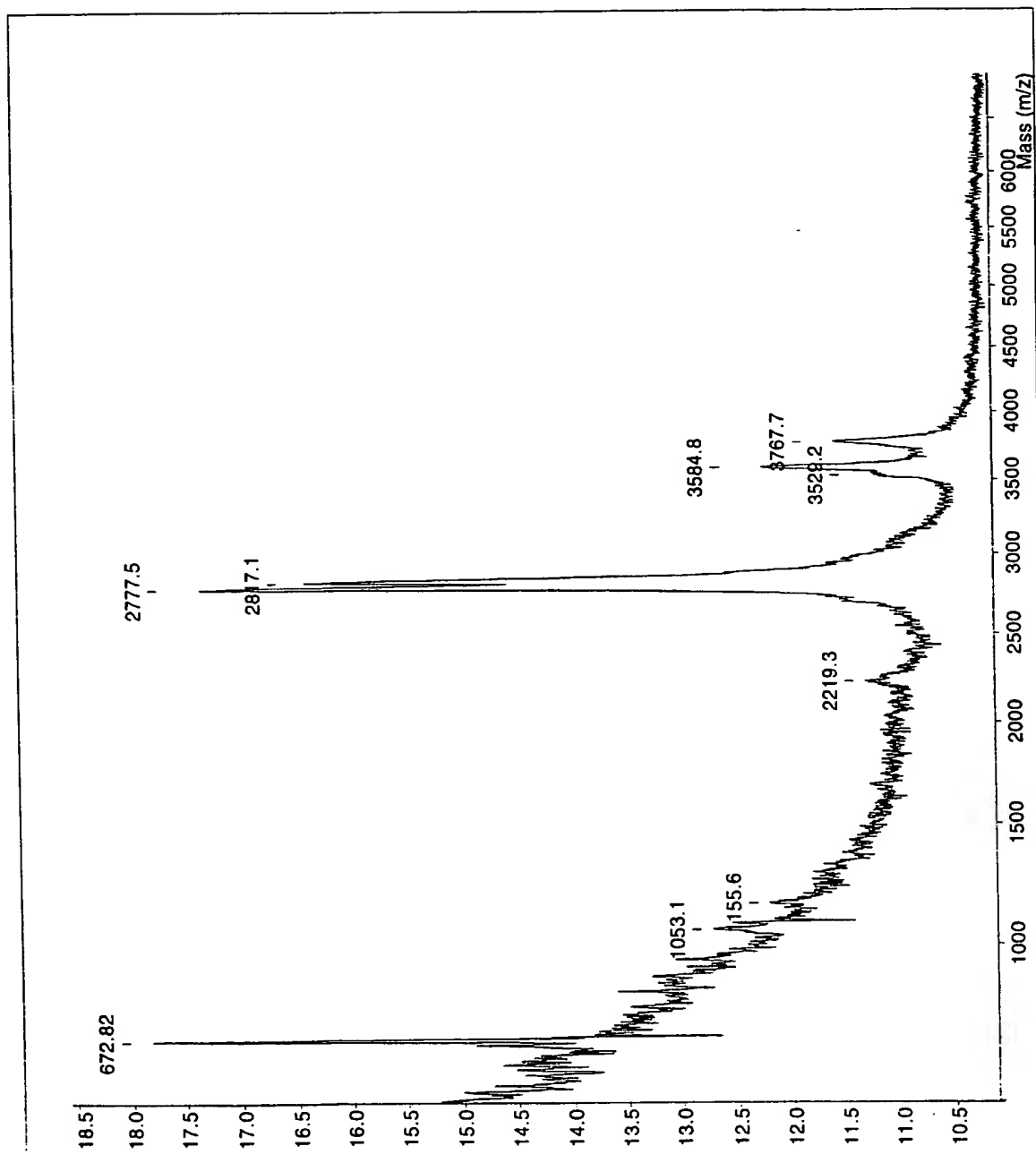
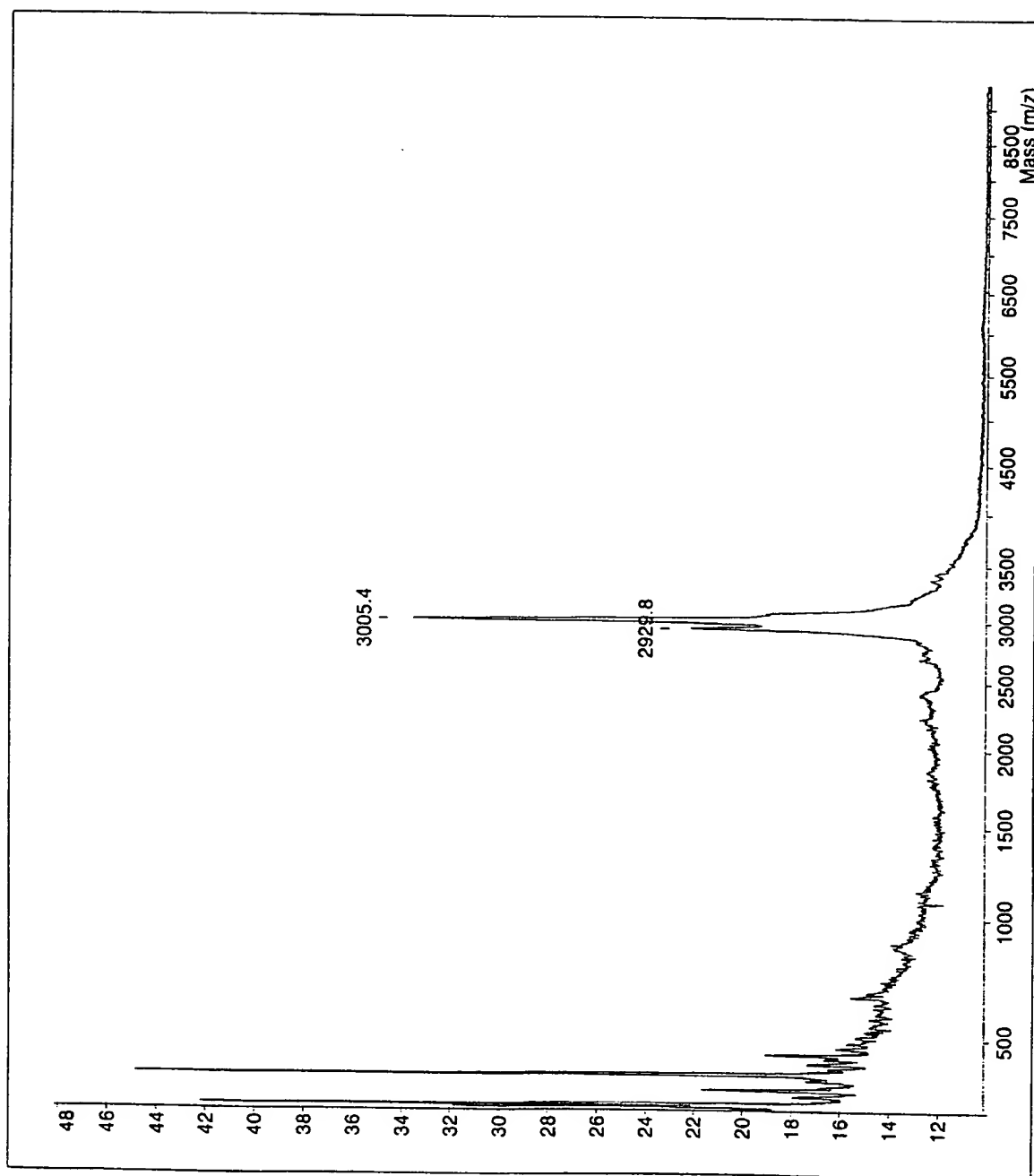


FIG. 5C

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FIG. 5D



1 49 (intact hOC)

7 30 (fragment 7-30)

6 30 (fragment 6-30)

fraction number	fragment lenght	determined mass	amino acid sequence	γ-carboxylated glutamic acid residues
43	N. D.	2778	not determined	1 -3 residues
44	7-30	2814	GAPVPYPDPLGlaPRRGlaVCGlaLNPD	17, 21 and 24
46	6-30	2930	LGAPVPYPDPLGlaPRRGlaVCGlaLNPD	17, 21 and 24
47	N.D.	3005	not determined	1 -3 residues

FIG. 5E

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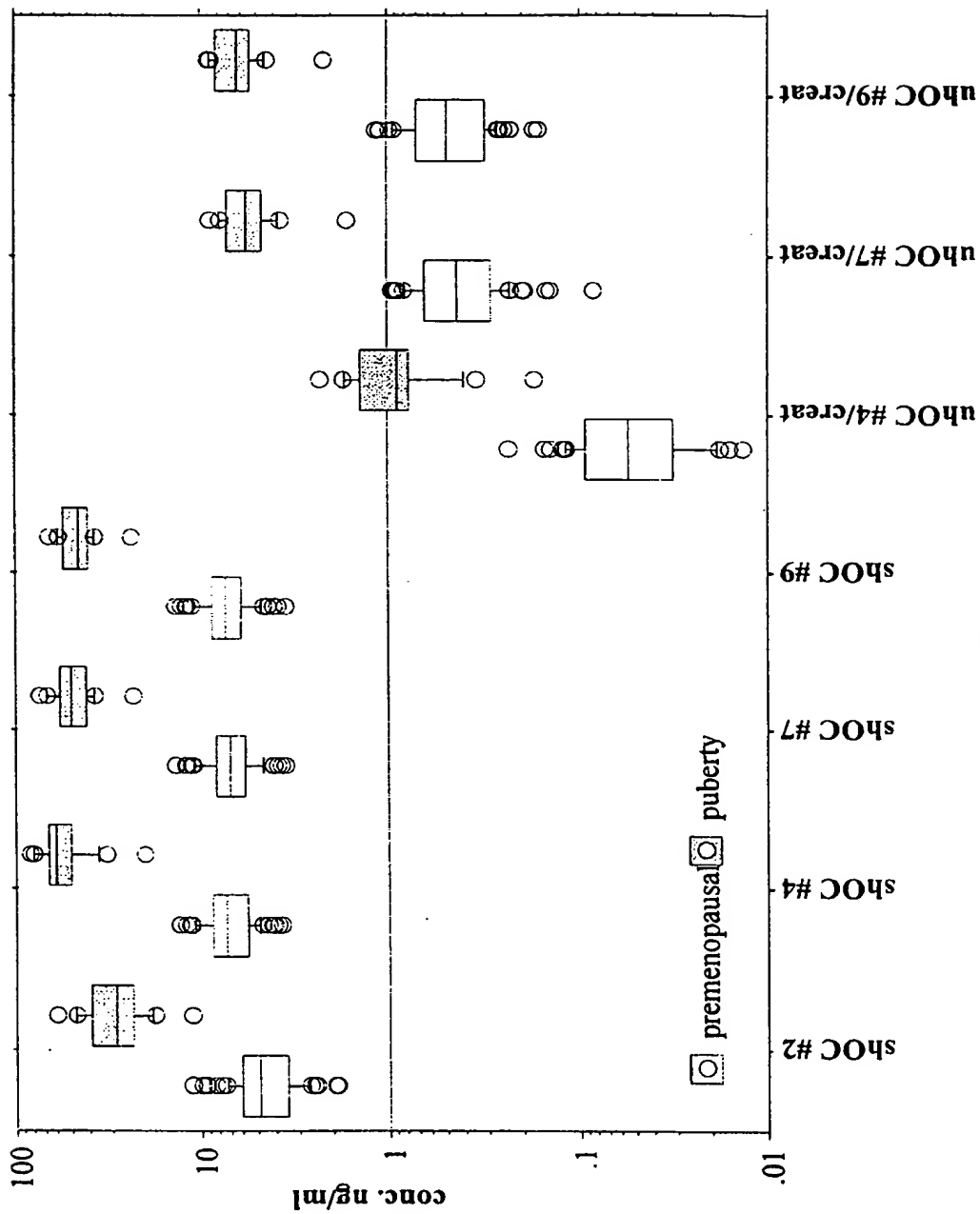


FIG 6

FIG 6

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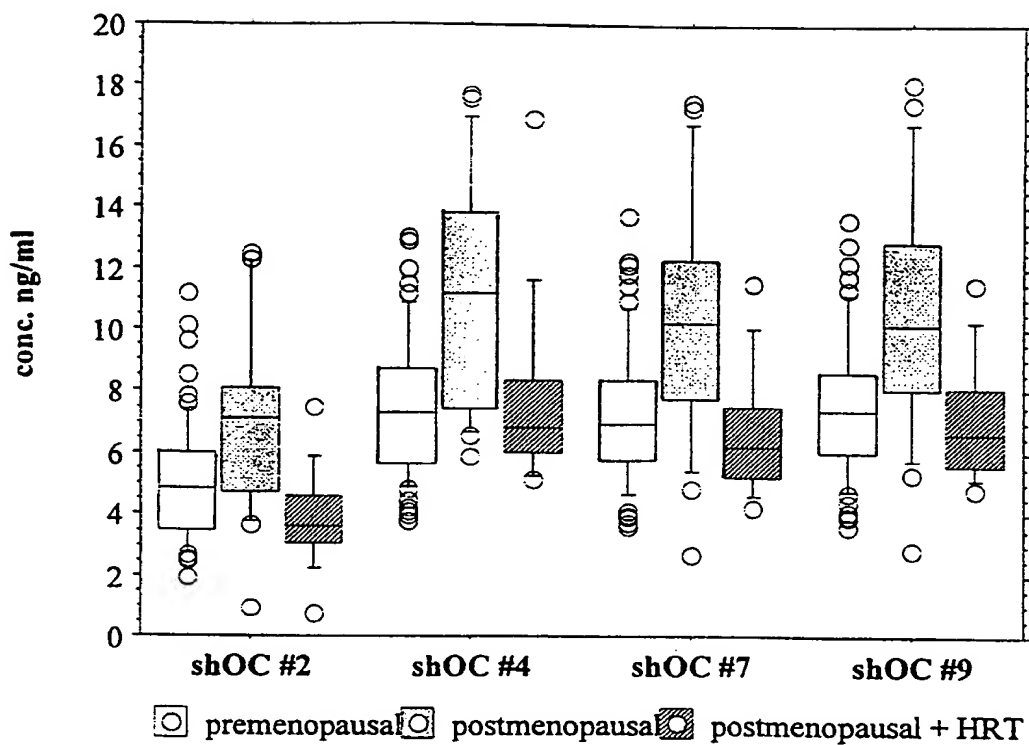


FIG. 7A

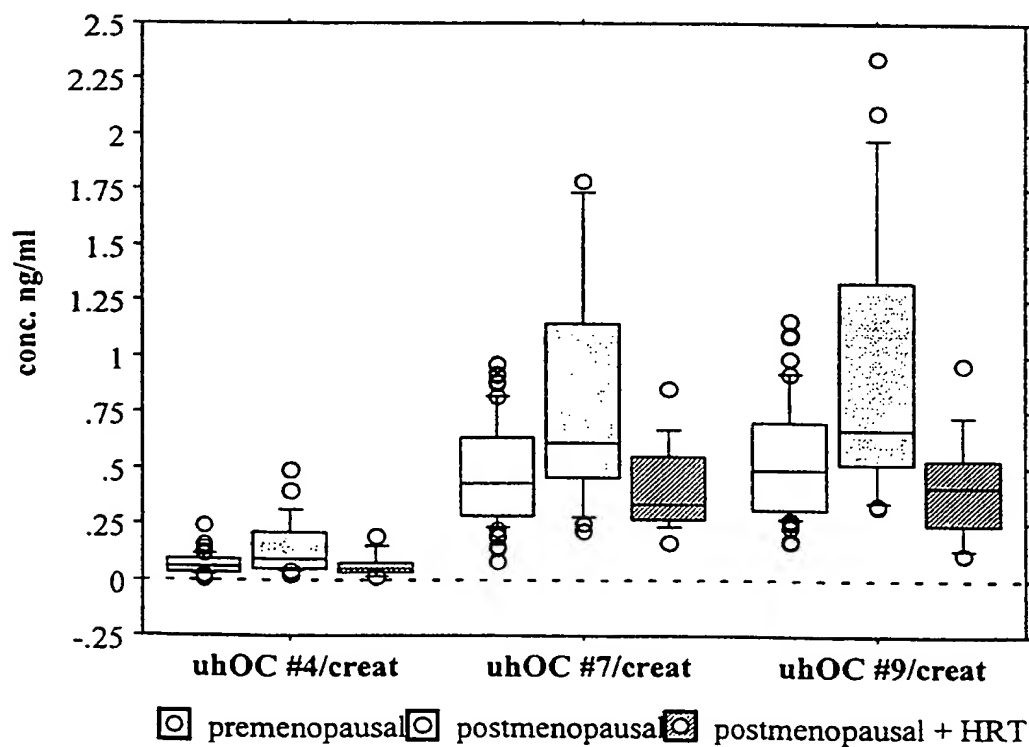
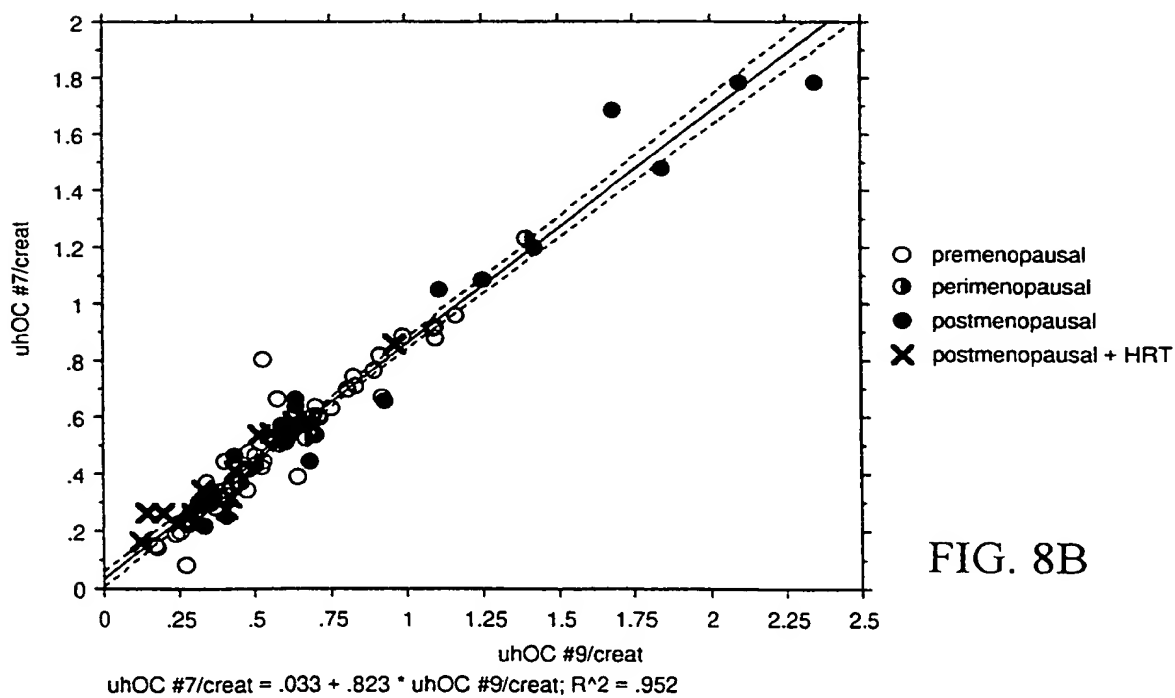
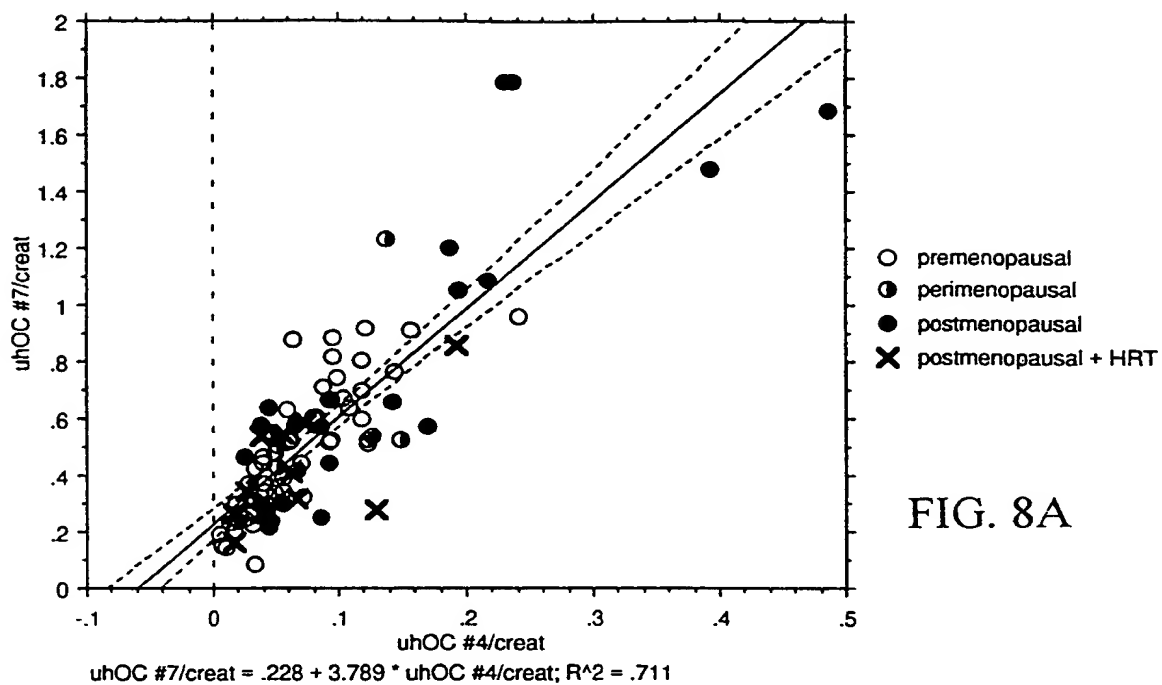


FIG. 7B

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